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## RAW SEQUENCE LISTING

DATE: 01/26/2002

PATENT APPLICATION: US/09/988,200

TIME: 14:03:42

Input Set : N:\Crf3\RULE60\09988200.raw

Output Set: N:\CRF3\01252002\I988200.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: BARBEYRON, Tristan

6 POTIN, Philippe

7 RICHARD, Christophe

8 HENRISSAT, Bernard

9 YVIN, Jean-Claude

10 KLOAREG, Bernard

13 (ii) TITLE OF INVENTION: Glycolyse hydrolase genes and their  
 14 use for producing enzymes for the biodegradation of  
 15 carrageenans

17 (iii) NUMBER OF SEQUENCES: 8

19 (iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: DENNISON, MESEROLE, SCHEINER &amp; SCHULTZ

21 (B) STREET: 612 Crystal Square 4, 1745 Jefferson Davis  
 22 Highway

23 (C) CITY: ARLINGTON

24 (D) STATE: VIRGINIA

25 (E) COUNTRY: U.S.A.

26 (F) ZIP: 22202

28 (v) COMPUTER READABLE FORM:

29 (A) MEDIUM TYPE: Floppy disk

30 (B) COMPUTER: IBM PC compatible

31 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

32 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

34 (vi) CURRENT APPLICATION DATA:

C--&gt; 35 (A) APPLICATION NUMBER: US/09/988,200

C--&gt; 36 (B) FILING DATE: 19-Nov-2001

37 (C) CLASSIFICATION:

43 (vii) PRIOR APPLICATION DATA:

40 (A) APPLICATION NUMBER: 09/269,731

41 (B) FILING DATE:

44 (A) APPLICATION NUMBER: FR 96 12204

45 (B) FILING DATE: 07-OCT-1996

47 (viii) ATTORNEY/AGENT INFORMATION:

48 (A) NAME: IRA SCHULTZ

49 (B) REGISTRATION NUMBER:

50 (C) REFERENCE/DOCKET NUMBER:

52 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: (703) 412 1155

54 (B) TELEFAX: (703) 412-1161

56 (2) INFORMATION FOR SEQ ID NO: 1:

58 (i) SEQUENCE CHARACTERISTICS:

ENTERED

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59      (A) LENGTH: 2085 base pairs
60      (B) TYPE: nucleic acid
61      (C) STRANDEDNESS: single
62      (D) TOPOLOGY: linear
64      (ii) MOLECULE TYPE: DNA (genomic)
66      (iii) HYPOTHETICAL: NO
70      (ix) FEATURE:
71          (A) NAME/KEY: CDS
72          (B) LOCATION: join(211..1683, 1880..2083)
74      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
76 AAGCTTTCCG ATTCTATCAT CGAAGTCATA GGAGTGGGTA AACAAAAAAG CATGAAACTA      60
77 GCTTTTTTAAA ATACAGACTT TCAATATAGG TCGCACACAA TATTAACGAA TAAATAAGCA      120
78 AATCATATAC ATAATCATTG CTTTAAATAT GTTTTAATAC AGATATAAAC ATAGTATGTT      180
79 TGTGTTTTTG GTATCTATCG GAGTGAAAC ATG CGC TTA TAT TTT AGA AAG TTG      234
80                                     Met Arg Leu Tyr Phe Arg Lys Leu
81                                     1           5
83 TGG TTA ACA AAT TTA TTT TTA GGC GGA GCA CTG GCC TCT TCA GCT GCG      282
84 Trp Leu Thr Asn Leu Phe Leu Gly Gly Ala Leu Ala Ser Ser Ala Ala
85      10           15           20
87 ATA GGG GCT GTC TCC CCC AAG ACT TAT AAG GAC GCA GAT TTT TAT GTT      330
88 Ile Gly Ala Val Ser Pro Lys Thr Tyr Lys Asp Ala Asp Phe Tyr Val
89      25           30           35           40
91 GCC CCT ACT CAA CAA GAT GTT AAC TAT GAT TTA GTT GAT GAT TTT GGC      378
92 Ala Pro Thr Gln Asp Val Asn Tyr Asp Leu Val Asp Asp Phe Gly
93      45           50           55
95 GCT AAT GGA AAC GAC ACT AGT GAT GAC AGT AAT GCT TTA CAA AGA GCA      426
96 Ala Asn Gly Asn Asp Thr Ser Asp Asp Ser Asn Ala Leu Gln Arg Ala
97      60           65           70
99 ATT AAT GCT ATT AGT AGA AAA CCG AAT GGG GGC ACT TTA CTA ATA CCG      474
100 Ile Asn Ala Ile Ser Arg Lys Pro Asn Gly Gly Thr Leu Leu Ile Pro
101      75           80           85
103 AAT GGA ACT TAC CAT TTC CTC GGC ATA CAG ATG AAG TCG AAC GTA CAC      522
104 Asn Gly Thr Tyr His Phe Leu Gly Ile Gln Met Lys Ser Asn Val His
105      90           95           100
107 ATC CGT GTT GAG AGT GAC GTG ATA ATC AAG CCA ACG TGG AAT GGG GAT      570
108 Ile Arg Val Glu Ser Asp Val Ile Ile Lys Pro Thr Trp Asn Gly Asp
109 105           110           115           120
111 GGC AAA AAC CAC CGA CTA TTT GAA GTT GGC GTA AAC AAT ATT GTA AGA      618
112 Gly Lys Asn His Arg Leu Phe Glu Val Gly Val Asn Asn Ile Val Arg
113      125           130           135
115 AAC TTC AGC TTT CAA GGG TTA GGA AAC GGT TTT TTG GTG GAT TTT AAA      666
116 Asn Phe Ser Phe Gln Gly Leu Gly Asn Gly Phe Leu Val Asp Phe Lys
117      140           145           150
119 GAT TCT CGC GAC AAA AAC TTA GCT GTT TTT AAG TTA GGC GAT GTT AGA      714
120 Asp Ser Arg Asp Lys Asn Leu Ala Val Phe Lys Leu Gly Asp Val Arg
121      155           160           165
123 AAT TAC AAA ATT TCC AAT TTT ACC ATT GAT GAT AAT AAA ACG ATA TTT      762
124 Asn Tyr Lys Ile Ser Asn Phe Thr Ile Asp Asp Asn Lys Thr Ile Phe
125      170           175           180

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|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |      |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| 127 | GCC | TCA | ATT | TTA | GTG | GAC | GTA | ACA | GAA | CGT | AAT | GGG | CGG | TTA | CAT | TGG | 810  |
| 128 | Ala | Ser | Ile | Leu | Val | Asp | Val | Thr | Glu | Arg | Asn | Gly | Arg | Leu | His | Trp |      |
| 129 | 185 |     |     |     |     | 190 |     |     |     | 195 |     |     |     |     |     | 200 |      |
| 131 | TCG | CGT | AAT | GGA | ATT | ATC | GAA | AGA | ATA | AAA | CAA | AAT | AAC | GCT | TTG | TTC | 858  |
| 132 | Ser | Arg | Asn | Gly | Ile | Ile | Glu | Arg | Ile | Lys | Gln | Asn | Asn | Ala | Leu | Phe |      |
| 133 |     |     |     |     | 205 |     |     |     |     | 210 |     |     |     |     |     | 215 |      |
| 135 | GGC | TAC | GGC | CTT | ATT | CAA | ACC | TAT | GGC | GCA | GAT | AAT | ATT | TTG | TTT | AGG | 906  |
| 136 | Gly | Tyr | Gly | Leu | Ile | Gln | Thr | Tyr | Gly | Ala | Asp | Asn | Ile | Leu | Phe | Arg |      |
| 137 |     |     |     | 220 |     |     |     |     |     | 225 |     |     |     |     |     | 230 |      |
| 139 | AAC | CTC | CAT | TCG | GAA | GGC | GGA | ATT | CGG | TTA | CGG | ATG | GAA | ACT | GAC | AAC | 954  |
| 140 | Asn | Leu | His | Ser | Glu | Gly | Gly | Ile | Ala | Leu | Arg | Met | Glu | Thr | Asp | Asn |      |
| 141 |     |     | 235 |     |     |     |     | 240 |     |     |     |     |     |     |     | 245 |      |
| 143 | TTA | CTT | ATG | AAA | AAT | TAT | AAG | CAA | GGC | GGA | ATA | AGA | AAC | ATC | TTT | GCT | 1002 |
| 144 | Leu | Leu | Met | Lys | Asn | Tyr | Lys | Gln | Gly | Gly | Ile | Arg | Asn | Ile | Phe | Ala |      |
| 145 |     | 250 |     |     |     |     |     | 255 |     |     |     |     |     |     |     | 260 |      |
| 147 | GAT | AAT | ATC | AGA | TGT | AGC | AAA | GGA | CTT | GCG | GCG | GTC | ATG | TTT | GGC | CCA | 1050 |
| 148 | Asp | Asn | Ile | Arg | Cys | Ser | Lys | Gly | Leu | Ala | Ala | Val | Met | Phe | Gly | Pro |      |
| 149 | 265 |     |     |     |     |     | 270 |     |     |     |     | 275 |     |     |     | 280 |      |
| 151 | CAT | TTT | ATG | AAG | AAT | GGA | GAT | GTG | CAA | GTG | ACC | AAT | GTC | AGC | TCA | GTT | 1098 |
| 152 | His | Phe | Met | Lys | Asn | Gly | Asp | Val | Gln | Val | Thr | Asn | Val | Ser | Ser | Val |      |
| 153 |     |     |     |     | 285 |     |     |     |     | 290 |     |     |     |     |     | 295 |      |
| 155 | AGT | TGC | GGT | TCG | GCT | GTA | CGA | AGT | GAT | AGT | GGA | TTT | GTC | GAA | CTC | TTT | 1146 |
| 156 | Ser | Cys | Gly | Ser | Ala | Val | Arg | Ser | Asp | Ser | Gly | Phe | Val | Glu | Leu | Phe |      |
| 157 |     |     |     | 300 |     |     |     |     |     | 305 |     |     |     |     |     | 310 |      |
| 159 | AGC | CCG | ACA | GAC | GAA | GTA | CAT | ACG | CGT | CAA | AGT | TGG | AAA | CAA | GCC | GTT | 1194 |
| 160 | Ser | Pro | Thr | Asp | Glu | Val | His | Thr | Arg | Gln | Ser | Trp | Lys | Gln | Ala | Val |      |
| 161 |     |     | 315 |     |     |     |     | 320 |     |     |     |     |     |     |     | 325 |      |
| 163 | GAA | AGT | AAA | TTG | GGC | CGA | GGG | TGT | GCG | CAA | ACC | CCT | TAT | GCT | AGA | GGT | 1242 |
| 164 | Glu | Ser | Lys | Leu | Gly | Arg | Gly | Cys | Ala | Gln | Thr | Pro | Tyr | Ala | Arg | Gly |      |
| 165 |     | 330 |     |     |     |     |     | 335 |     |     |     |     |     |     |     | 340 |      |
| 168 | AAT | GGT | GGT | ACA | CGG | TGG | GCG | GCT | CGC | GTA | ACA | CAA | AAA | GAC | GCG | TGT | 1290 |
| 169 | Asn | Gly | Gly | Thr | Arg | Trp | Ala | Ala | Arg | Val | Thr | Gln | Lys | Asp | Ala | Cys |      |
| 170 | 345 |     |     |     |     | 350 |     |     |     |     |     | 355 |     |     |     | 360 |      |
| 172 | TTA | GAT | AAA | GCA | AAA | CTG | GAA | TAT | GGA | ATA | GAG | CCT | GGT | TCA | TTT | GGC | 1338 |
| 173 | Leu | Asp | Lys | Ala | Lys | Leu | Glu | Tyr | Gly | Ile | Glu | Pro | Gly | Ser | Phe | Gly |      |
| 174 |     |     |     |     | 365 |     |     |     |     | 370 |     |     |     |     |     | 375 |      |
| 176 | ACG | GTT | AAA | GTC | TTT | GAT | GTT | ACA | GCG | CGT | TTT | GGT | TAT | AAC | GCA | GAT | 1386 |
| 177 | Thr | Val | Lys | Val | Phe | Asp | Val | Thr | Ala | Arg | Phe | Gly | Tyr | Asn | Ala | Asp |      |
| 178 |     |     |     | 380 |     |     |     |     |     | 385 |     |     |     |     |     | 390 |      |
| 180 | CTT | AAA | CAG | GAC | CAG | CTA | GAC | TAC | TTT | TCT | ACA | TCC | AAC | CCT | ATG | TGC | 1434 |
| 181 | Leu | Lys | Gln | Asp | Gln | Leu | Asp | Tyr | Phe | Ser | Thr | Ser | Asn | Pro | Met | Cys |      |
| 182 |     |     | 395 |     |     |     |     | 400 |     |     |     |     |     |     |     | 405 |      |
| 184 | AAG | CGT | GTA | TGC | CTT | CCT | ACA | AAA | GAA | CAA | TGG | AGT | AAG | CAA | GGC | CAA | 1482 |
| 185 | Lys | Arg | Val | Cys | Leu | Pro | Thr | Lys | Glu | Gln | Trp | Ser | Lys | Gln | Gly | Gln |      |
| 186 |     | 410 |     |     |     |     |     | 415 |     |     |     |     |     |     |     | 420 |      |
| 188 | ATT | TAC | ATT | GGT | CCG | TCA | TTA | GCT | GCA | GTA | ATT | GAT | ACC | ACA | CCT | GAA | 1530 |
| 189 | Ile | Tyr | Ile | Gly | Pro | Ser | Leu | Ala | Ala | Val | Ile | Asp | Thr | Thr | Pro | Glu |      |
| 190 | 425 |     |     |     |     | 430 |     |     |     |     |     | 435 |     |     |     | 440 |      |
| 192 | ACT | TCA | AAA | TAC | GAT | TAT | GAT | GTG | AAA | ACT | TTT | AAC | GTC | AAA | AGA | ATA | 1578 |

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193 Thr Ser Lys Tyr Asp Tyr Asp Val Lys Thr Phe Asn Val Lys Arg Ile
194          445          450          455
196 AAT TTT CCT GTA AAT TCA CAC AAG ACT ATC GAC ACG AAT ACT GAA AGT      1626
197 Asn Phe Pro Val Asn Ser His Lys Thr Ile Asp Thr Asn Thr Glu Ser
198          460          465          470
200 AGC CGT GTC TGC AAT TAT TAC GGT ATG TCC GAA TGC TCC AGC AGT CGA      1674
201 Ser Arg Val Cys Asn Tyr Tyr Gly Met Ser Glu Cys Ser Ser Ser Arg
202          475          480          485
204 TGG GAG CGA TAGATTAAGC CGCTATATTC ATTTACTAGG TAAAACTTCA      1723
205 Trp Glu Arg
206          490
208 AGCCGCATTC GAAGAACTAT CGAACGCGGC TTTTGTGTTA AGAGCGCCTA TGA CTCAGTA      1783
209 TATTTTGTAT AAATATAATT TTACATCTTG TTAAAGTAAA CATCATATGT TTATATAGGT      1843
210 GCAATCTAAT TTGTTAATAT AGTGTGAG ATAGGT ATG AAA GGT GTT TCT ACG      1897
211          Met Lys Gly Val Ser Thr
212          495
215 AAA AAT GCT CTT TTA TTT GCA GGC TTT TCG TTA AGT CTA GTT GCA CAG      1945
216 Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala Gln
217          500          505          510
219 TCA GTT AGT GCA CAA GAA GCA AAA CAG CCT GAA AAA GAA GAA AAA GAT      1993
220 Ser Val Ser Ala Gln Glu Ala Lys Gln Pro Glu Lys Glu Glu Lys Asp
221          515          520          525
223 GTT GAG GTG ATT TTG GTA TCG GCA CAA AAG CGT GAG CAA GCG CTT AAA      2041
224 Val Glu Val Ile Leu Val Ser Ala Gln Lys Arg Glu Gln Ala Leu Lys
225 530          535          540          545
227 GAA GTG CCT GTA TCA ATT GAA GTT ATT CAA GGC GAC CTT CTA GA      2085
228 Glu Val Pro Val Ser Ile Glu Val Ile Gln Gly Asp Leu Leu
229          550          555
232 (2) INFORMATION FOR SEQ ID NO: 2:
234 (i) SEQUENCE CHARACTERISTICS:
235 (A) LENGTH: 559 amino acids
236 (B) TYPE: amino acid
237 (D) TOPOLOGY: linear
239 (ii) MOLECULE TYPE: protein
241 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
243 Met Arg Leu Tyr Phe Arg Lys Leu Tip Leu Thr Asn Leu Phe Leu Gly
244 1          5          10          15
245 Gly Ala Leu Ala Ser Ser Ala Ala Ile Gly Ala Val Ser Pro Lys Thr
246          20          25          30
247 Tyr Lys Asp Ala Asp Phe Tyr Val Ala Pro Thr Gln Gln Asp Val Asn
248          35          40          45
249 Tyr Asp Leu Val Asp Asp Phe Gly Ala Asn Gly Asn Asp Thr Ser Asp
250          50          55          60
251 Asp Ser Asn Ala Leu Gln Arg Ala Ile Asn Ala Ile Ser Arg Lys Pro
252 65          70          75          80
253 Asn Gly Gly Thr Leu Leu Ile Pro Asn Gly Thr Tyr His Phe Leu Gly
254          85          90          95
255 Ile Gln Met Lys Ser Asn Val His Ile Arg Val Glu Ser Asp Val Ile
256          100          105          110

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257 Ile Lys Pro Thr Trp Asn Gly Asp Gly Lys Asn His Arg Leu Phe Glu
258      115      120      125
259 Val Gly Val Asn Asn Ile Val Arg Asn Phe Ser Phe Gln Gly Leu Gly
260      130      135      140
263 Asn Gly Phe Leu Val Asp Phe Lys Asp Ser Arg Asp Lys Asn Leu Ala
264 145      150      155      160
265 Val Phe Lys Leu Gly Asp Val Arg Asn Tyr Lys Ile Ser Asn Phe Thr
266      165      170      175
267 Ile Asp Asp Asn Lys Thr Ile Phe Ala Ser Ile Leu Val Asp Val Thr
268      180      185      190
269 Glu Arg Asn Gly Arg Leu His Trp Ser Arg Asn Gly Ile Ile Glu Arg
270      195      200      205
271 Ile Lys Gln Asn Asn Ala Leu Phe Gly Tyr Gly Leu Ile Gln Thr Tyr
272      210      215      220
273 Gly Ala Asp Asn Ile Leu Phe Arg Asn Leu His Ser Glu Gly Gly Ile
274 225      230      235      240
275 Ala Leu Arg Met Glu Thr Asp Asn Leu Leu Met Lys Asn Tyr Lys Gln
276      245      250      255
277 Gly Gly Ile Arg Asn Ile Phe Ala Asp Asn Ile Arg Cys Ser Lys Gly
278      260      265      270
279 Leu Ala Ala Val Met Phe Gly Pro His Phe Met Lys Asn Gly Asp Val
280      275      280      285
281 Gln Val Thr Asn Val Ser Ser Val Ser Cys Gly Ser Ala Val Arg Ser
282      290      295      300
283 Asp Ser Gly Phe Val Glu Leu Phe Ser Pro Thr Asp Glu Val His Thr
284 305      310      315      320
285 Arg Gln Ser Trp Lys Gln Ala Val Glu Ser Lys Leu Gly Arg Gly Cys
286      325      330      335
287 Ala Gln Thr Pro Tyr Ala Arg Gly Asn Gly Gly Thr Arg Trp Ala Ala
288      340      345      350
289 Arg Val Thr Gln Lys Asp Ala Cys Leu Asp Lys Ala Lys Leu Glu Tyr
290      355      360      365
291 Gly Ile Glu Pro Gly Ser Phe Gly Thr Val Lys Val Phe Asp Val Thr
292      370      375      380
293 Ala Arg Phe Gly Tyr Asn Ala Asp Leu Lys Gln Asp Gln Leu Asp Tyr
294 385      390      395      400
295 Phe Ser Thr Ser Asn Pro Met Cys Lys Arg Val Cys Leu Pro Thr Lys
296      405      410      415
297 Glu Gln Trp Ser Lys Gln Gly Gln Ile Tyr Ile Gly Pro Ser Leu Ala
298      420      425      430
299 Ala Val Ile Asp Thr Thr Pro Glu Thr Ser Lys Tyr Asp Tyr Asp Val
300      435      440      445
301 Lys Thr Phe Asn Val Lys Arg Ile Asn Phe Pro Val Asn Ser His Lys
302      450      455      460
303 Thr Ile Asp Thr Asn Thr Glu Ser Ser Arg Val Cys Asn Tyr Tyr Gly
304 465      470      475      480
305 Met Ser Glu Cys Ser Ser Ser Arg Trp Glu Arg Met Lys Gly Val Ser
306      485      490      495
307 Thr Lys Asn Ala Leu Leu Phe Ala Gly Phe Ser Leu Ser Leu Val Ala

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Output Set: N:\CRF3\01252002\I988200.raw

L:35 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:36 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]